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RECEIVED Page 1 of 7 #18

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TECH CENTER 1600/2900

1638

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/945,144A DATE: 11/07/2000
TIME: 11:38:40

Input Set : A:\Rpmu5e.app
Output Set: N:\CRF3\11072000\H945144A.raw

3 <110> APPLICANT: Lebrun, Michel
4 Sailland, Alain
5 Freyssinet, Georges
6 DeGryse, Eric
8 <120> TITLE OF INVENTION: Mutated 5-Enol Pyruvylshikimate-3-Phosphate Synthase,
9 Gene Coding for Said Protein and Transformed Plants
10 Containing Said Gene
12 <130> FILE REFERENCE: 5500-13
14 <140> CURRENT APPLICATION NUMBER: 08/945,144A
15 <141> CURRENT FILING DATE: 1998-01-20
17 <150> PRIOR APPLICATION NUMBER: PCT/FR96/01125
18 <151> PRIOR FILING DATE: 1996-07-18
20 <150> PRIOR APPLICATION NUMBER: FRANCE 95/08979
21 <151> PRIOR FILING DATE: 1995-07-19
23 <160> NUMBER OF SEQ ID NOS: 15
25 <170> SOFTWARE: PatentIn Ver. 2.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1713
29 <212> TYPE: DNA
30 <213> ORGANISM: Zea mays
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37 ccatcaaggaa gatctccggc accgtcaacg tgcgggggtc caagtccgtt tccaaaccgg 180
39 tcctctact cggccgcctg tccgagggga caacagtggt tgataaacctg ctgaacagt 240
41 aggatgtcc ctacatgctc ggggccttgc ggacttctgg tctctctgtc gaagcggaca 300
43 aagctgcca aagagctgtt gttgttggtt gtgggtggaa gtcccaggat gaggatgtca 360
45 aagagagaat gcagcttcc ttggggatgtt ctggaaatgc aatycggcca ttgacagcag 420
47 ctgttactgc tgctgtgttgc aatgcactt acgtgtttgc ttggatccca aqaatgaggg 480
49 agagacccat tggcgacttgc gttgtcgat tgaacgttgc ttgtgttgc 540
51 tccttggcac tgacttccca cctgttgc tcaatggat cggagggtca cttgggtggca 600
53 aaggtaaact gtttgttgc accacccatgc agtacttgc tgcccttgc atggctgtc 660
55 cttyggcttc tggggatgtt gagatgtttt ttcattgttata attaaatctcc attccgttacg 720
57 tccaaatgttcc attggatgtt atggagcgtt ttgtgttgc agcagagcat tctgtatgt 780
59 gggacagatt ctacattaag ggaggtcaaa aatacaagtc ccctaaaaat gcctatgtt 840
61 aagggttatgc ctcaagcgtca agcttgc tgcatttttgc tgqcttgc tgcatttttgc 900
63 tgactgttgc aggttgttgc accacccatgc tgccgttgc ttgtgttgc ttgtgttgc 960
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67 cgcggggacc accacccatgc tggggatgtt accacccatgc tgccgttgc ttgtgttgc 1080
69 ctgtatgttgc ctatgttgc tgcatttttgc cccttttgc tgcatttttgc ttgtgttgc 1140
71 gagacgttgc ttcttggaga taaaaggaga ccgagaggat ggttgtgc tgcatttttgc 1200
73 taacccatgc gggagcgttgc tgcatttttgc tgccgttgc ttgtgttgc ttgtgttgc 1260
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77 cccttgcgtcc ctgttgc tggggatgtt accacccatgc tggggatgtt accacccatgc tgccgttgc ttgtgttgc 1380
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83 ctgttttttgc ctgttgc tggggatgtt accacccatgc tggggatgtt accacccatgc tgccgttgc ttgtgttgc 1560

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85 tttctatttc ggatcttaag tttgtgcact gtaagccaaa ttcatatca agagtggttc 1620
87 gtggataaa taagaataat aaattacgtt tcagtaaaaa aaaaaaaaaa aaaaaaaaaa 1680
89 aaaaaaaaaa aaaaaaaaaa aacccgggaa ttc 1713
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93 <211> LENGTH: 1340
94 <212> TYPE: DNA
95 <213> ORGANISM: Zea mays
97 <220> FEATURE:
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99 <222> LOCATION: (6)..(1337)
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104     1           5           10          15
106 ggc acc gtc aag ctg ccc ggg tcc aag tcg ctt tcc aac cgg atc ctc  98
107 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
108             20          25          30
110 cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146
111 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu
112             35          40          45
114 aac agt gag gat gtc cac tac atg ctc ggg gcc ttg agg act ctt ggt 194
115 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
116             50          55          60
118 ctc tct gtc gaa gcg gac aaa gct gcc aaa aga gct gta gtt gtt ggc 242
119 Leu Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly
120             65          70          75
122 tgt ggt gga aag ttc cca gtt gag gat gct aaa gag gaa gtg cag ctc 290
123 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
124   80          85          90          95
126 ttc ttg ggg aat gct gya act gca atg cgg cca ttg aca gca gct gtt 338
127 Phe Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val
128             100         105         110
130 act gct gct ggt gga aat gca act tac gtg ctt gat gga gta cca aga 386
131 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
132             115         120         125
134 atg agg gag aga ccc att ggc gac ttg gtc gga ttg aag cag ctt 434
135 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
136             130         135         140
138 ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt 482
139 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
140             145         150         155
142 gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc 530
143 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly
144   160          165          170          175
146 tcc atc agc agt cag tac ttg agt gcc ttg ctg atg gct gct cct ttg 578
147 Ser Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu
148             180          185          190
150 gct ctt ggg gat gtg gag att gaa atc att gat aaa tta atc tcc att 626
151 Ala Leu Gly Asp Val Glu Ile Glu Ile Asp Lys Leu Ile Ser Ile

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152	195	200	205	
154	ccg tac gtc gaa atg aca ttg aga ttg atg gag cgt ttt ggt gtg aac			674
155	Pro Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys			
156	210	215	220	
158	gca gag cat tct gat agc tgg gac aga ttc tac att aag gga ggt caa			722
159	Ala Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln			
160	225	230	235	
162	aaa tac aag tcc cct aaa aat gcc tat gtt gaa ggt gat gcc tca agc			770
163	Lys Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser			
164	240	245	250	255
166	gca aqc tat ttc ttg gct ggt gct gca att act gga ggg act gtq act			818
167	Ala Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr			
168	260	265	270	
170	gtg gaa ggt tqt ggc acc acc agt ttg cag ggt gat gtg aag tt.t gct			866
171	Val Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala			
172	275	280	285	
174	gag gta ctg gag atg atg gga gca aag gtt aca tgg acc gag act agc			914
175	Glu Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser			
176	290	295	300	
178	gta act qtt act ggc cca ccg cgg gag cca ttt ggg agg aaa cac ctc			962
179	Val Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu			
180	305	310	315	
182	aag gcg att gat gtc aac atg aac aag atg cct gat gtc gcc atg act			1010
183	Lys Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr			
184	320	325	330	335
186	ctt gct gtg ttg gcc ctc ttt gcc gat ggc ccg aca gcc atc aga gac			1058
187	Leu Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp			
188	340	345	350	
190	gtg gct tcc tgg aga gta aag gag acc gag agg atg gtt gcg atc cgg			1106
191	Val Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg			
192	355	360	365	
194	acg gag cta acc aag ctg gga gca tct gtt gag gaa ggg cgg qac tac			1154
195	Thr Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr			
196	370	375	380	
198	tgc atc atc acg ccg ccg gag aag ctg aac gtg acg gcg atc gac acg			1202
199	Cys Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr			
200	385	390	395	
202	tac gac gac cac agg atg gcc atg ttc tcc ctt gcc gcc tgt gcc			1250
203	Tyr Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala			
204	400	405	410	415
206	gag gtc ccc gtc acc atc cgg gac cct ggg tgc acc cgg aag acc ttc			1298
207	Glu Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe			
208	420	425	430	
210	ccc gac tac ttc gat gtg ctg agc act ttc gtc aag aat taa			1340
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216	<211> LENGTH: 444			
217	<212> TYPE: PRT			

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218 <213> ORGANISM: Zea mays
220 <400> SEQUENCE: 3
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225   20          25          30
227 Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn
228   35          40          45
230 Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu
231   50          55          60
233 Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Val Gly Cys
234   65          70          75          80
236 Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Glu Leu Phe
237   85          90          95
239 Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
240   100         105         110
242 Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
243   115         120         125
245 Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
246   130         135         140
248 Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val
249   145         150         155         160
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252   165         170         175
254 Ile Ser Ser Gln Tyr Leu Ser Ala Leu Met Ala Ala Pro Leu Ala
255   180         185         190
257 Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro
258   195         200         205
260 Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala
261   210         215         220
263 Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gly Gln Lys
264   225         230         235         240
266 Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala
267   245         250         255
269 Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val
270   260         265         270
272 Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu
273   275         280         285
275 Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val
276   290         295         300
278 Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys
279   305         310         315         320
281 Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu
282   325         330         335
284 Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val
285   340         345         350
287 Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr
288   355         360         365
290 Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys

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291      370          375          380
293 Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr
294 385          390          395          400
296 Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu
297          405          410          415
299 Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro
300          420          425          430
302 Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn
303          435          440
306 <210> SEQ ID NO: 4
307 <211> LENGTH: 1340
308 <212> TYPE: DNA
309 <213> ORGANISM: Zea mays
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (6)..(1337)
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318     1           5           10          15
320 ggc acc gtc aag ctg ccc ggg tcc aag tcc ctt tcc aac cgg atc ctc  98
321 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu
322     20          25          30
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326     35          40          45
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329 Asn Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly
330     50          55          60
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334     65          70          75
336 tgt ggt gga aag ttc cca gtc gat gat gct aaa gag gaa gtg cag ctc 290
337 Cys Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu
338     80          85          90          95
340 ttc ttg ggg aat gct gga atc gca atg cgg tcc ttg aca gca gct gtt 338
341 Phe Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val
342     100         105         110
344 act gct gct ggt gga aat gca act tac gtc ctt gat gga gta cca aga 386
345 Thr Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg
346     115         120         125
348 atg agg gag aga ccc att ggc gac ttg gtt gtc gga ttg aag cag ctt 434
349 Met Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu
350     130         135         140
352 ggt gca gat gtt gat tgt ttc ctt ggc act gac tgc cca cct gtt cgt 482
353 Gly Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg
354     145         150         155
356 gtc aat gga atc gga ggg cta cct ggt ggc aag gtc aag ctg tct ggc 530
357 Val Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly

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VERIFICATION SUMMARY
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